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RAW SEQUENCE LISTING

DATE: 12/18/2003

PATENT APPLICATION: US/09/611,419B

TIME: 14:53:05

Input Set : A:\09611419ThirdSubSeqList.txt

Output Set: N:\CRF4\12182003\I611419B.raw

3 <110> APPLICANT: Smith, Leonard A.
 4 Byrne, Michael P.
 5 Middlebrook, John L.
 6 Lapenotiere, Hugh
 7 Clayton, Michael A.
 8 Brown, Douglas R.
 10 <120> TITLE OF INVENTION: RECOMBINANT VACCINE AGAINST BOTULINUM
 11 NEUROTOXIN
 13 <130> FILE REFERENCE: A33626 067252.0105
 15 <140> CURRENT APPLICATION NUMBER: 09/611,419B
 16 <141> CURRENT FILING DATE: 2000-07-06
 18 <150> PRIOR APPLICATION NUMBER: PCT/US00/12890
 19 <151> PRIOR FILING DATE: 2000-05-12
 21 <150> PRIOR APPLICATION NUMBER: 60/133,865
 22 <151> PRIOR FILING DATE: 1999-05-12
 24 <150> PRIOR APPLICATION NUMBER: 60/133,866
 25 <151> PRIOR FILING DATE: 1999-05-12
 27 <150> PRIOR APPLICATION NUMBER: 60/133,867
 28 <151> PRIOR FILING DATE: 1999-05-12
 30 <150> PRIOR APPLICATION NUMBER: 60/133,868
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 33 <150> PRIOR APPLICATION NUMBER: 60/133,869
 34 <151> PRIOR FILING DATE: 1999-05-12
 36 <150> PRIOR APPLICATION NUMBER: 60/146,192
 37 <151> PRIOR FILING DATE: 1999-07-29
 39 <150> PRIOR APPLICATION NUMBER: 08/123,975
 40 <151> PRIOR FILING DATE: 1993-09-21
 42 <160> NUMBER OF SEQ ID NOS: 44
 44 <170> SOFTWARE: FastSEQ for Windows Version 4.0
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 47 <211> LENGTH: 1332
 48 <212> TYPE: DNA
 49 <213> ORGANISM: Artificial Sequence
 51 <220> FEATURE:
 52 <223> OTHER INFORMATION: Synthetic construct based on BoNTA Hc
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 56 acctccatcc tgaacctgcg ctacgaatcc aatcacctga tcgacctgtc tcgctacgct 120
 57 tccaaaatca acatcggttc taaagttaac ttcgatccga tcgacaagaa tcagatccag 180
 58 ctgttcaatc tggaatcttc caaaatcgaa gttatcctga agaattgctat cgtatacaac 240
 59 tctatgtacg aaaacttctc cacctccttc tggatccgta tcccgaataa cttcaactcc 300
 60 atctctctga acaatgaata caccatcatc aactgcatgg aaaacaattc tgggttgaaa 360
 61 gtatctctga actacggtga aatcatctgg actctgcagg acactcagg aatcaaacag 420

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63 ttcgttacca tcaccaacaa tcgtctgaat aactccaaaa tctacatcaa cggccgtctg 540
64 atcgaccaga aaccgatctc caatctgggt aacatccacg cttctaataa catcatgttc 600
65 aaactggacg gttgtcgtga cactcaccgc tacatctgga tcaaatactt caatctgttc 660
66 gacaaagaac tgaacgaaaa agaaatcaaa gacctgtacg acaaccagtc caattctggt 720
67 atcctgaaag acttctgggg tgactacctg cagtacgaca aaccgtacta catgctgaat 780
68 ctgtacgatc cgaacaaata cggtgacgac aacaatgtag gtatccgcgg ttacatgtac 840
69 ctgaaaggtc cgcgtgggtc tggtatgact accaacaatc acctgaactc ttccctgtac 900
70 cgtggtacca aattcatcat caagaaatac gcgtctggta acaaggacaa tatcgttcgc 960
71 aacaatgatc gtgtatacat caatgttgta gttagaaca aagaataaccg tctggctacc 1020
72 aatgcttctc aggtcgggtg agaaaagatc ttgtctgctc tggaaatccc ggacgttggt 1080
73 aatctgtctc aggtagttgt aatgaaatcc aagaacgacc agggatatcac taacaaatgc 1140
74 aaaatgaatc tgcaggacaa caatggtaac gatatcggtt tcatcggttt ccaccagttc 1200
75 aacaatcgcg ctaaactggt tgcttccaac tggatcaatc gtcagatcga acgttcctct 1260
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82 <213> ORGANISM: Artificial Sequence
84 <220> FEATURE:
85 <223> OTHER INFORMATION: Encoded polypeptide of a synthetic construct based
86 on BoNTA Hc
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91 Thr Ser Ile Leu Asn Leu Arg Tyr Glu Ser Asn His Leu Ile Asp Leu
92 20 25 30
93 Ser Arg Tyr Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp
94 35 40 45
95 Pro Ile Asp Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys
96 50 55 60
97 Ile Glu Val Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu
98 65 70 75 80
99 Asn Phe Ser Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser
100 85 90 95
101 Ile Ser Leu Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn
102 100 105 110
103 Ser Gly Trp Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu
104 115 120 125
105 Gln Asp Thr Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln
106 130 135 140
107 Met Ile Asn Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile
108 145 150 155 160
109 Thr Asn Asn Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu
110 165 170 175
111 Ile Asp Gln Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn
112 180 185 190
113 Asn Ile Met Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile

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115 Trp Ile Lys Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu
116          210          215          220
117 Ile Lys Asp Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp
118 225          230          235          240
119 Phe Trp Gly Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn
120          245          250          255
121 Leu Tyr Asp Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg
122          260          265          270
123 Gly Tyr Met Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn
124          275          280          285
125 Ile Tyr Leu Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys
126          290          295          300
127 Lys Tyr Ala Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg
128 305          310          315          320
129 Val Tyr Ile Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr
130          325          330          335
131 Asn Ala Ser Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile
132          340          345          350
133 Pro Asp Val Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn
134          355          360          365
135 Asp Gln Gly Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn
136          370          375          380
137 Gly Asn Asp Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala
138 385          390          395          400
139 Lys Leu Val Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser
140          405          410          415
141 Arg Thr Leu Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp
142          420          425          430
143 Gly Glu Arg Pro Leu
144          435
147 <210> SEQ ID NO: 3
148 <211> LENGTH: 1323
149 <212> TYPE: DNA
150 <213> ORGANISM: Artificial Sequence
152 <220> FEATURE:
153 <223> OTHER INFORMATION: Synthetic construct based on BoNTA Hc
155 <400> SEQUENCE: 3
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157 ctgaacctgc gctacgaatc caatcacctg atcgacctgt ctcgctacgc ttccaaaatc 120
158 aacatcgggt ctaaagttaa cttcgatccg atcgacaaga atcagatcca gctgttcaat 180
159 ctggaatctt ccaaaatcga agttatcctg aagaatgcta tcgtatacaa ctctatgtac 240
160 gaaaacttct ccacctcctt ctggatccgt atcccgaat acttcaactc catctctctg 300
161 aacaatgaat acaccatcat caactgcatg gaaaacaatt ctggttgga agtatctctg 360
162 aactacggtg aaatcatctg gactctgcag gacactcagg aaatcaaaca gcgtgttgta 420
163 ttcaataact ctcagatgat caacatctct gactacatca atcgctggat cttcgttacc 480
164 atcaccaaca atcgtctgaa taactccaaa atctacatca acggccgtct gatcgaccag 540
165 aaaccgatct ccaatctggg taacatccac gcttctaata acatcatgtt caaactggac 600
166 ggttgctctg acactcaccg ctacatctgg atcaaatact tcaatctgtt cgacaaagaa 660

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167 ctgaacgaaa aagaaatcaa agacctgtac gacaaccagt ccaattctgg tatcctgaaa 720
168 gacttctggg gtgactacct gcagtacgac aaaccgtact acatgctgaa tctgtacgat 780
169 ccgaacaaat acgttgacgt caacaatgta ggtatccgcg gttacatgta cctgaaaggt 840
170 ccgcgtgggt ctgttatgac taccaacatc tacctgaact cttccctgta ccgtgggtacc 900
171 aaattcatca tcaagaaata cgcgtctggt aacaaggaca atatcgttcg caacaatgat 960
172 cgtgtatata tcaatgttgt agttaagaac aaagaataacc gtctggctac caatgcttct 1020
173 caggctgggt tagaaaagat ctgtctgtct ctggaaatcc cggacgttgg taatctgtct 1080
174 caggtagttg taatgaaatc caagaacgac cagggtatca ctaacaaatg caaatgaat 1140
175 ctgcaggaca acaatggtaa cgatatcggt ttcacggtt tccaccagtt caacaatatc 1200
176 gctaaactgg ttgcttccaa ctggtacaat cgtcagatcg aacgttcctc tcgcactctg 1260
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181 <211> LENGTH: 434

182 <212> TYPE: PRT

183 <213> ORGANISM: Artificial Sequence

185 <220> FEATURE:

186 <223> OTHER INFORMATION: Encoded polypeptide of a synthetic construct based
 187 on BoNTA Hc

189 <400> SEQUENCE: 4

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193 20 25 30
194 Ala Ser Lys Ile Asn Ile Gly Ser Lys Val Asn Phe Asp Pro Ile Asp
195 35 40 45
196 Lys Asn Gln Ile Gln Leu Phe Asn Leu Glu Ser Ser Lys Ile Glu Val
197 50 55 60
198 Ile Leu Lys Asn Ala Ile Val Tyr Asn Ser Met Tyr Glu Asn Phe Ser
199 65 70 75 80
200 Thr Ser Phe Trp Ile Arg Ile Pro Lys Tyr Phe Asn Ser Ile Ser Leu
201 85 90 95
202 Asn Asn Glu Tyr Thr Ile Ile Asn Cys Met Glu Asn Asn Ser Gly Trp
203 100 105 110
204 Lys Val Ser Leu Asn Tyr Gly Glu Ile Ile Trp Thr Leu Gln Asp Thr
205 115 120 125
206 Gln Glu Ile Lys Gln Arg Val Val Phe Lys Tyr Ser Gln Met Ile Asn
207 130 135 140
208 Ile Ser Asp Tyr Ile Asn Arg Trp Ile Phe Val Thr Ile Thr Asn Asn
209 145 150 155 160
210 Arg Leu Asn Asn Ser Lys Ile Tyr Ile Asn Gly Arg Leu Ile Asp Gln
211 165 170 175
212 Lys Pro Ile Ser Asn Leu Gly Asn Ile His Ala Ser Asn Asn Ile Met
213 180 185 190
214 Phe Lys Leu Asp Gly Cys Arg Asp Thr His Arg Tyr Ile Trp Ile Lys
215 195 200 205
216 Tyr Phe Asn Leu Phe Asp Lys Glu Leu Asn Glu Lys Glu Ile Lys Asp
217 210 215 220
218 Leu Tyr Asp Asn Gln Ser Asn Ser Gly Ile Leu Lys Asp Phe Trp Gly

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219 225          230          235          240
220 Asp Tyr Leu Gln Tyr Asp Lys Pro Tyr Tyr Met Leu Asn Leu Tyr Asp
221          245          250          255
222 Pro Asn Lys Tyr Val Asp Val Asn Asn Val Gly Ile Arg Gly Tyr Met
223          260          265          270
224 Tyr Leu Lys Gly Pro Arg Gly Ser Val Met Thr Thr Asn Ile Tyr Leu
225          275          280          285
226 Asn Ser Ser Leu Tyr Arg Gly Thr Lys Phe Ile Ile Lys Lys Tyr Ala
227          290          295          300
228 Ser Gly Asn Lys Asp Asn Ile Val Arg Asn Asn Asp Arg Val Tyr Ile
229 305          310          315          320
230 Asn Val Val Val Lys Asn Lys Glu Tyr Arg Leu Ala Thr Asn Ala Ser
231          325          330          335
232 Gln Ala Gly Val Glu Lys Ile Leu Ser Ala Leu Glu Ile Pro Asp Val
233          340          345          350
234 Gly Asn Leu Ser Gln Val Val Val Met Lys Ser Lys Asn Asp Gln Gly
235          355          360          365
236 Ile Thr Asn Lys Cys Lys Met Asn Leu Gln Asp Asn Asn Gly Asn Asp
237          370          375          380
238 Ile Gly Phe Ile Gly Phe His Gln Phe Asn Asn Ile Ala Lys Leu Val
239 385          390          395          400
240 Ala Ser Asn Trp Tyr Asn Arg Gln Ile Glu Arg Ser Ser Arg Thr Leu
241          405          410          415
242 Gly Cys Ser Trp Glu Phe Ile Pro Val Asp Asp Gly Trp Gly Glu Arg
243          420          425          430
244 Pro Leu
248 <210> SEQ ID NO: 5
249 <211> LENGTH: 1326
250 <212> TYPE: DNA
251 <213> ORGANISM: Artificial Sequence
253 <220> FEATURE:
254 <223> OTHER INFORMATION: Synthetic construct based on BoNTA Hc
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259 atcaacatcg gttctaaaagt taacttcgat ccgatcgaca agaatcagat ccagctgttc 180
260 aatctggaat cttccaaaat cgaagttatc ctgaagaatg ctatcgata caactctatg 240
261 tacgaaaact tctccacctc cttctggatc cgtatcccga aatacttcaa ctccatctct 300
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263 ctgaactacg gtgaaatcat ctggactctg caggacactc aggaaatcaa acagcgtgtt 420
264 gtattcaaat actctcagat gatcaacatc tctgactaca tcaatcgctg gatcttcgtt 480
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267 gacggttgtc gtgacactca ccgctacatc tggatcaaat acttcaatct gttcgacaaa 660
268 gaactgaacg aaaaagaaat caaagacctg tacgacaacc agtccaattc tggtatcctg 720
269 aaagacttct ggggtgacta cctgcagtac gacaaaccgt actacatgct gaatctgtac 780
270 gatccgaaca aatacgttga cgtcaacaat gtaggtatcc gcggttacat gtacctgaaa 840
271 ggtccgcgtg gttctgttat gactaccaac atctacctga actcttcctt gtaccgtggg 900
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VERIFICATION SUMMARY

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